SEQUENCE LISTING

<110> PIERRE FABRE MÉDICAMENT

<120> USE OF AN ENTEROBACTERIUM OmpA PROTEIN FOR SPECIFIC TARGETING OF A BIOLOGICALLY ACTIVE SUBSTANCE WHICH IS ASSOCIATED WITH IT TO ANTIGEN-PRESENTING CELLS

<130> D17777

<140>
<141>

<150> FR 98 14007
<151> 1998-11-06

<160> 2

<170> PatentIn Ver. 2.2

<210> 1
<211> 1035
<212> ADN
<213> Klebsiella pneumoniae

<220>
<221> exon
<222> (1)..(1032)

<220>
<221> intron
<222> (1033)..(1035)

<220>
<221> CDS
<222> (1)..(1032)

<400> 1

```
atg aaa gca att ttc gta ctg aat gcg gct ccg aaa gat aac acc tgg   48
Met Lys Ala Ile Phe Val Leu Asn Ala Ala Pro Lys Asp Asn Thr Trp
  1               5                  10                  15

tat gca ggt ggt aaa ctg ggt tgg tcc cag tat cac gac acc ggt ttc   96
Tyr Ala Gly Gly Lys Leu Gly Trp Ser Gln Tyr His Asp Thr Gly Phe
             20                  25                  30

tac ggt aac ggt ttc cag aac aac aac ggt ccg acc cgt aac gat cag   144
Tyr Gly Asn Gly Phe Gln Asn Asn Asn Gly Pro Thr Arg Asn Asp Gln
         35                  40                  45

ctt ggt gct ggt gcg ttc ggt ggt tac cag gtt aac ccg tac ctc ggt   192
Leu Gly Ala Gly Ala Phe Gly Gly Tyr Gln Val Asn Pro Tyr Leu Gly
     50                  55                  60

ttc gaa atg ggt tat gac tgg ctg ggc cgt atg gca tat aaa ggc agc   240
Phe Glu Met Gly Tyr Asp Trp Leu Gly Arg Met Ala Tyr Lys Gly Ser
 65                  70                  75                  80

gtt gac aac ggt gct ttc aaa gct cag ggc gtt cag ctg acc gct aaa   288
Val Asp Asn Gly Ala Phe Lys Ala Gln Gly Val Gln Leu Thr Ala Lys
```

```
                    85                  90                  95

ctg ggt tac ccg atc act gac gat ctg gac atc tac acc cgt ctg ggc   336
Leu Gly Tyr Pro Ile Thr Asp Asp Leu Asp Ile Tyr Thr Arg Leu Gly
            100                 105                 110

ggc atg gtt tgg cgc gct gac tcc aaa ggc aac tac gct tct acc ggc   384
Gly Met Val Trp Arg Ala Asp Ser Lys Gly Asn Tyr Ala Ser Thr Gly
        115                 120                 125

gtt tcc cgt agc gaa cac gac act ggc gtt tcc cca gta ttt gct ggc   432
Val Ser Arg Ser Glu His Asp Thr Gly Val Ser Pro Val Phe Ala Gly
    130                 135                 140

ggc gta gag tgg gct gtt act cgt gac atc gct acc cgt ctg gaa tac   480
Gly Val Glu Trp Ala Val Thr Arg Asp Ile Ala Thr Arg Leu Glu Tyr
145                 150                 155                 160

cag tgg gtt aac aac atc ggc gac gcg ggc act gtg ggt acc cgt cct   528
Gln Trp Val Asn Asn Ile Gly Asp Ala Gly Thr Val Gly Thr Arg Pro
                165                 170                 175

gat aac ggc atg ctg agc ctg ggc gtt tcc tac cgc ttc ggt cag gaa   576
Asp Asn Gly Met Leu Ser Leu Gly Val Ser Tyr Arg Phe Gly Gln Glu
            180                 185                 190

gat gct gca ccg gtt gtt gct ccg gct ccg gct ccg gct ccg gaa gtg   624
Asp Ala Ala Pro Val Val Ala Pro Ala Pro Ala Pro Ala Pro Glu Val
        195                 200                 205

gct acc aag cac ttc acc ctg aag tct gac gtt ctg ttc aac ttc aac   672
Ala Thr Lys His Phe Thr Leu Lys Ser Asp Val Leu Phe Asn Phe Asn
    210                 215                 220

aaa gct acc ctg aaa ccg gaa ggt cag cag gct ctg gat cag ctg tac   720
Lys Ala Thr Leu Lys Pro Glu Gly Gln Gln Ala Leu Asp Gln Leu Tyr
225                 230                 235                 240

act cag ctg agc aac atg gat ccg aaa gac ggt tcc gct gtt gtt ctg   768
Thr Gln Leu Ser Asn Met Asp Pro Lys Asp Gly Ser Ala Val Val Leu
                245                 250                 255

ggc tac acc gac cgc atc ggt tcc gaa gct tac aac cag cag ctg tct   816
Gly Tyr Thr Asp Arg Ile Gly Ser Glu Ala Tyr Asn Gln Gln Leu Ser
            260                 265                 270

gag aaa cgt gct cag tcc gtt gtt gac tac ctg gtt gct aaa ggc atc   864
Glu Lys Arg Ala Gln Ser Val Val Asp Tyr Leu Val Ala Lys Gly Ile
        275                 280                 285

ccg gct ggc aaa atc tcc gct cgc ggc atg ggt gaa tcc aac ccg gtt   912
Pro Ala Gly Lys Ile Ser Ala Arg Gly Met Gly Glu Ser Asn Pro Val
    290                 295                 300

act ggc aac acc tgt gac aac gtg aaa gct cgc gct gcc ctg atc gat   960
Thr Gly Asn Thr Cys Asp Asn Val Lys Ala Arg Ala Ala Leu Ile Asp
305                 310                 315                 320

tgc ctg gct ccg gat cgt cgt gta gag atc gaa gtt aaa ggc tac aaa  1008
Cys Leu Ala Pro Asp Arg Arg Val Glu Ile Glu Val Lys Gly Tyr Lys
                325                 330                 335
```

gaa gtt gta act cag ccg gcg ggt taa 1035
Glu Val Val Thr Gln Pro Ala Gly
340

<210> 2
<211> 344
<212> PRT
<213> Klebsiella pneumoniae

<400> 2
Met Lys Ala Ile Phe Val Leu Asn Ala Ala Pro Lys Asp Asn Thr Trp
1 5 10 15

Tyr Ala Gly Gly Lys Leu Gly Trp Ser Gln Tyr His Asp Thr Gly Phe
20 25 30

Tyr Gly Asn Gly Phe Gln Asn Asn Asn Gly Pro Thr Arg Asn Asp Gln
35 40 45

Leu Gly Ala Gly Ala Phe Gly Gly Tyr Gln Val Asn Pro Tyr Leu Gly
50 55 60

Phe Glu Met Gly Tyr Asp Trp Leu Gly Arg Met Ala Tyr Lys Gly Ser
65 70 75 80

Val Asp Asn Gly Ala Phe Lys Ala Gln Gly Val Gln Leu Thr Ala Lys
85 90 95

Leu Gly Tyr Pro Ile Thr Asp Asp Leu Asp Ile Tyr Thr Arg Leu Gly
100 105 110

Gly Met Val Trp Arg Ala Asp Ser Lys Gly Asn Tyr Ala Ser Thr Gly
115 120 125

Val Ser Arg Ser Glu His Asp Thr Gly Val Ser Pro Val Phe Ala Gly
130 135 140

Gly Val Glu Trp Ala Val Thr Arg Asp Ile Ala Thr Arg Leu Glu Tyr
145 150 155 160

Gln Trp Val Asn Asn Ile Gly Asp Ala Gly Thr Val Gly Thr Arg Pro
165 170 175

Asp Asn Gly Met Leu Ser Leu Gly Val Ser Tyr Arg Phe Gly Gln Glu
180 185 190

Asp Ala Ala Pro Val Val Ala Pro Ala Pro Ala Pro Ala Pro Glu Val
195 200 205

Ala Thr Lys His Phe Thr Leu Lys Ser Asp Val Leu Phe Asn Phe Asn
210 215 220

Lys Ala Thr Leu Lys Pro Glu Gly Gln Gln Ala Leu Asp Gln Leu Tyr
225 230 235 240

Thr Gln Leu Ser Asn Met Asp Pro Lys Asp Gly Ser Ala Val Val Leu
245 250 255

Gly Tyr Thr Asp Arg Ile Gly Ser Glu Ala Tyr Asn Gln Gln Leu Ser

260 265 270

Glu Lys Arg Ala Gln Ser Val Val Asp Tyr Leu Val Ala Lys Gly Ile
275 280 285

Pro Ala Gly Lys Ile Ser Ala Arg Gly Met Gly Glu Ser Asn Pro Val
290 295 300

Thr Gly Asn Thr Cys Asp Asn Val Lys Ala Arg Ala Ala Leu Ile Asp
305 310 315 320

Cys Leu Ala Pro Asp Arg Arg Val Glu Ile Glu Val Lys Gly Tyr Lys
325 330 335

Glu Val Val Thr Gln Pro Ala Gly
340